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										APPLICANT Pandit					
										FILING DATE 03/31/2004			GROUP		
U.S. PATENT DOCUMENTS															
EXAMINER INITIAL		DOCUMENT NUMBER							DATE	NAME	CLASS	SUBCLASS	FILING DATE IF APPROPRIATE		
NN	US	4	6	8	3	1	9	5	07/28/87	Mullis, et al.	435/6	435/91			
NN	US	6	3	5	6	8	4	5	03/12/02	Benson, et al.	702/19	435/183			
FOREIGN PATENT DOCUMENTS															
		DOCUMENT NUMBER							DATE	COUNTRY	CLASS	SUBCLASS	TRANSLATION		
													YES	NO	
NN	CA	2	0	1	2	3	1	1	03/15/89	Canada	C12N	15/87			
NN	EP	1	0	8	5	0	9	2	03/21/01	Europe	C12N	15/53			
NN	WO	9	9	4	2	5	9	6	08/26/99	PCT	C12N	15/55			
OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages, Etc.)															
NN			Appelt, K., <i>Crystal structures of HIV-1 protease-inhibitor complexes</i> , <u>Perspectives in Drug Discovery and Design</u> , Vol. 1: 23-48, 1993												
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			Brooks, B., et al., <i>CHARMM: A program for macromolecular energy, minimization, and dynamics calculations</i> , <u>Journal of Comp. Chem.</u> , Vol. 4(2): 187-217, 1983												
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EXAMINER /Nasbaat Nashed/ (06/22/2006) DATE CONSIDERED															
<small>EXAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609; Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.</small>															

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DOCUMENT NUMBER	DATE	COUNTRY	CLASS	SUBCLASS	TRANSLATION	
					YES	NO

OTHER DOCUMENTS (Including Author, Title, Date, Pertinent Pages, Etc.)						
NN			Juarez-Martinez, G., et al., <i>High-throughput screens for postgenomics: studies of protein crystallization using Microsystems technology</i> , <u>Anal. Chem.</u> , Vol. 74: 3505-3510, 2002			
			Kabsch, W., et al., <i>Dictionary of protein secondary structure: pattern recognition of hydrogen-bonded and geometrical features</i> , <u>Biopolymers</u> , Vol. 22: 2577-2637, 1983			
			Kissinger, C., et al., <i>Rapid automated molecular replacement by evolutionary search</i> , <u>Acta Crystallographica</u> , Vol. D55: 484-491, 1999			
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			Murshudov, G., et al., <i>Refinement of Macromolecular structures by the maximum-likelihood method</i> , <u>Acta Cryst.</u> , Vol. D53: 240-255, 1997			
			Navaza, J., <i>AmoRe: an automated package for molecular replacement</i> , <u>Acta Crystallographica</u> , Vol. A50: 157-63, 1994			
			Otwinowski, Z., et al., <i>Processing of X-Ray diffraction data collected in oscillation mode</i> , <u>Methods in Enzymology</u> , Vol. 276: 307-326, 1997			
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